of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

resistance to plant disease, better growth rate by modification

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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
61 QYRVIDPKRNKDGIPGRVATIEYDPNRSANIALINYADGEKR--YIIAAKGLEVGQTIYS 118
                                                                                                 GAEADTKVGNALPLQNIPVGTVVHNIELKPGKGGQIARSAGASAQVLGKEGKYVLIRLRS 180
                                                                                                                                                                                                                                  181 GEVRMILSTCRATIGGVGNLQHELVNVGKAGRSRWKGIRPTVRGSVMNPNDHPHGGGEGR 240
                                                                                                                                                                                                                                                                     The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also rates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant source as some and a comprise transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
                                                                                                                                       119 GAEADIKVGNALELKDIPVGTVIHNIEMKPGKGGQLVRSAGTSAQVLGKEGKYVLIRLNS
                                                                                                                                                                                                                                                                                                                                                                   241 APIGRPSPMSPWGKPTLGKKTRRGKKSSDKLIVRGRKKK 279
                                                                                                                                                                                                                                                                                                                                                                                                         239 APIGRKSPMSPWGKPTLGYKTRKKNNNSDKFIVRRRKKK 277
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HINKLE G J.
SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-061375/06.
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(SLAT/)
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(GOLD/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
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ID ADS4

AC ADS4

AC ADS4

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                                                                                                                                                                                                                                                                                                                                                             61 OYRVIDFKRDKDGIPGRVATVEYDPNRSANIALINYADGEKR--YILAPKGIQVGTEIMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 GEVRMILSACRASIGQVGNEQHELINIGKAGRSRWKGIRPTVRGSVMNPNDHPHGGGEGR
                                                                                                                                                                                                                                                                                                                                                                                                                                      119 GPEADIKVGNALPLINIPVGTVVHNIELKPGKGGOLVRSAGTSAQVLGKEGKYVLVRLNS
                                                                                                                                                                                                                                                                                1 MAIKKYKPITNGRRNMTSLDFAEITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
                                                                                                                                                                                                                                                                                                                                           61 QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVES
                                                                                                                                                                                                                                                                                                                                                                                                       121 GAEADTKVGNALPLONIPVGTVVHNIELKPGKGGQIARSAGASAQVLGKEGKYVLIRLRS
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                                                                                                                                                                                                                Length 277;
                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 APIGRKSPMSPWGKPTLEFKTRKOKNKSDKFIVRRRKNK 277
                                                                                                                                                                                                               79.9%; Score 1163; DB 8;
79.9%; Pred. No. 6.8e-108;
iive 19; Mismatches 35;
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                                                                                                                                                                                                                                              Matches 223; Conservative
                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            completed: June
                                                                                                                                                                                   Sequence 277 AA;
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                                                                                                                                                                                                                  Query Match
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Antisense; prokaryotic essential gene; cell proliferation; drug design

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The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and to sopply the sist and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes. Talated diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the composition for Lesquences.
                                                                                                                                                                                                                                                                          Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related
                              Cossart P;
                       Checouni F, Nedjari H, Glaser P, Kunst F, Cossart F, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Ernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; T, Domann E, Hain T, Berche P, Charbit A, Durant L; J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
     Feihi H,
       Rusniok C,
                                                                                                                                                                                                                                                                                                                                                                            Claim 6; SEQ ID NO 2071; 192pp; French
     Frangeul L,
Chetouani F,
                                                                                                   Chakraborty T, Domann E,
Perez-Diaz J, Baquero F,
Maduenio E, De Pablos B,
                                                                                                                                                                                                                               WPI; 2002-010914/01.
                                                        Daniels J, Goebel W
Dominguez-Bernal G,
                                                                                                                                                                                Voss H;
Buchrieser C,
                                 Dussurget O,
                                                                                                                                                                                                                                                                                                                             polypeptides
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Sequence 277 AA;

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120
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                                                                                                                                                                              61 QYRVIDFKRNKDGIPGRVATIEYDFNRSANIALINYADGEKR--YIIAAKGLEVGQTIYS
                                                                             1 MAIKKYKPITNGRRNMTSLDFAEITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
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                                                                                                                                                            QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVES
                                                                                                                                                                                                                                       121 GAEADTKVGNALPLQNIPVGTVVHNIELKPGKGGQIARSAGASAQVLGKEGKYVLIRLRS
                                                                                                                                                                                                                                                                                                                  181 GEVRMILSTCRATIGQVGNLQHELVNVGKAGRSRWKGIRPTVRGSVMNPNDHPHGGGEGR
                                        2;
Length 277;
                                      27; Indels
                                                                                                                                                                                                                                                                                                                                                                                             241 APIGRPSPMSPWGKPTLGKKTRRGKKSSDKLIVRGRKKK 279
                                                                                                                                                                                                                                                                                                                                                                                                                     APIGRKSPMSPWGKPTLGYKTRKKNNNSDKFIVRRRKKK 277
82.6%; Score 1203; DB 5; ilarity 82.4%; Pred. No. 6.5e-112; Conservative 20; Mismatches 27;
              Best_Local_Similarity
Matches 230; Conserv
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  Query Match
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Protein encoded by Prokaryotic essential gene #18069.
                ABU32542 standard; protein; 277
                                                 19-JUN-2003 (first entry)
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the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

cenceding a polypeptide whose expression is inhibited by the antisense

concluding a polypeptide whose expression is inhibited by the antisense

concluding a polypeptide whose expression is inhibited by the antisense

contisense nucleic acid; (4) an antibody capable of specifically binding

contisense nucleic acid; (4) an antibody capable of specifically binding

contisense nucleic acid; (4) an antibody capable of specifically binding

contisense nucleic acid; (4) an antibody capable of specifically binding

contisense nucleic acid; (4) an antibody capable of specifically binding

contisense nucleic acid; (4) an antibody capable of specifically binding

contisense nucleic acid; (4) a mantibody capable of specifically binding

contisense nucleic acidi; (4) a mantibody capable of specifically binding

contisense nucleic acidity of a gene in an operon required for

contisense or that has an activity against a biological pathway

contisense or that has an activity against a biological pathway

confoured for proliferation, or that inhibits cellular proliferation of an

corganism acts; (9) manufacturing an antibiotic; (10) profiling a

congound's activity; (11) a culture comprising strains in which the gene

congound's activity; (11) a culture comprising strains in which the gene

conduct is overexpressed or underexpressed; (12) determining the extent

conduct is overexpressed or underexpressed; (12) determining the extent

conduct is overexpressed or underexpressed; (12) determining the extent

confounds; or (13) identifying the target of a compound that inhibits the

confounds; or (13) identifying the target of a compound that inhibits or collection of

confounds; or (13) identifying the target of a compound that inhibits capable are useful for

confounds or proliferation of an organism. The antisense mucleic acids are useful for

confound the acid or the proliferation of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, th. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAIKKYKPTTNGRRHWTSSDFAEITTSTPEKSLLRPLKKKAGRNNQGKLTVRHHGGGHKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAIKKYKPITNGRRNWTSLDFAEITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.6%; Score 1203; DB 6; Length 277; 82.4%; Pred. No. 6.5e-112; ive 20; Mismatches 27; Indels 5
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; SEQ ID NO 60466; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Malone C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carr GJ,
                                                                                                                                                                                                                                                              21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0192923P.
08-FEB-2002; 2002US-00672851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                               21-MAR-2002; 2002WO-US009107.
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Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           (ELIT-) ELITRA PHARM INC.
                                                    Listeria monocytogenes
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Trawick JD,
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Wall D,
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense encoding a polypeptide whose expression is inhibited by the antisense polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                           120
                                                                                                                                                        240
                                                                                                                                                                      61 QYRVIDFKRNKDGIIAKVDSIQYDPNRSANIALLVYADGEKR--YIIAPKGLQVGQTVES 118
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             MAIKKYKPITNGRRNMTSLDPAEITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
                          1 MALKKYKPITNGRRNMTTLDFAEITKTTPEKSLLQPLPKRAGRNNGKLTVRHHGGGHKR
                                                           61 QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVES
                                                                                                           121 GAEADTKVGNALPLONIPVGTVVHNIELKPGKGGQIARSAGASAQVLGKEGKYVLIRLRS
                                                                                                                                                        GEVRMILSTCRATIGOVGNLQHELVNVGKAGRSRWKGIRPTVRGSVMNPNDHPHGGGEGR
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                Protein encoded by Prokaryotic essential gene #28153
                                                                                                                                                                                                        241 APIGRPSPMSPWGKPTLGKKTRRGKKSSDKLIVRGRKKK 279
                                                                                                                                                                                                                     239 APIGRPSPMSPWGXPTLGKKTRRGKKSSDKLIVRGRKKK 277
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; SEQ ID NO 70550; 1766pp; English.
                                                                                                                                                                                                                                                                                          ABU42626 standard; protein; 277 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malone C,
Carr GJ,
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2001US-0342923P.
2002US-00072851.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                          19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ELIT-) ELITRA PHARM INC.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2003-029926/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200277183-A2.
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Wall D,
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the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) acquired for proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of the which each of the strains. The antisense mucleic acids are useful for proliferation of an organism. The antisense mucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. The traget prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the present sequence at the trained in the printed specification, but was obtained in the print proverse or the trained processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.3%; Score 1373; DB 6; 93.9%; Pred. No. 5.7e-129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Listeria monocytogenes protein #2070.
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Best Local Similarity
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06-MAR-2003 (first entry)
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Best Local Similarity 93.99
Matches 262; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meinke A, Nagy E, Vor
Minh DB, Vytvytska O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-075410/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200259148-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rempelmaier B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preparation
                                                                                                                                                                                                                                ABJ19022;
                                                                                                                                                       RESULT 11
                                                                                                                                                                         ABJ19022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an isolated nucleic acid comprising a nucleotide sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO: 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as given in the specification. Also described are: a recombinant expression vector of (1); producing an S. epidermidis polypeptide, an isolated nucleic acid comprising a nucleotide sequence of at least 8 nucleotides in length; a vaccine composition for prevention or treatment of an S. epidermidis infection, comprising a nucleic acid cited above and a carrier; treating a subject for S. epidermidis infection; a recombinant or substantially pure preparation of an S. epidermidis polypeptide or its fragment; a vaccine composition for prevention or treatment of an S. epidermidis infection; detecting the presence of a Staphylococcus nucleic acid in a sample; a computer readable medium having recorded in it the nucleotide sequences with SEQ ID NO: 1-3772 or its fragments; a computer based system for identifying fragments of the Staphylococcus genome of commercial importance; a computer based system for identifying fragments of the Staphylococcus genome of commercial importances and produced in interesting the presence of a computer pased system for identifying fragments of the Staphylococcus genome of commercial importance; a computer based system for identifying fragments of the Staphylococcus genome of commercial importances; a computer based system for identifying fragments of the staphylococcus genome of commercial importances and the staphylococcus genome of the staphylococcus genome of the staphylococcus genome of the staphylococcus successions and the staphyl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  commercially important nucleic acid fragments of the Staphylococcus genome and/or plasmids, and identifying an expression modulating fragment of the Staphylococcus genome and/or plasmids. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of an Staphylococcal epidermidis bacterial infection. This is the amino acid sequence of a S. epidermidis protein of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 QYRVIDFKRNKDGITAKVDSIQYDFNRSANIALLAVYADGEKR--YIIAPKGLQIGQTVES 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis, useful for disgnosing, preventing and/or treating an S. epidermidis bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polypeptide and encoding nucleic acid derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.4%; Score 1375; DB 8; Length 279; 93.5%; Pred. No. 3.6e-129; ive 12; Mismatches 4; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; SEQ ID NO 6371; 741pp; English.
                                                                                                                                                                                       98US-00134001.
                                                                                                                                01-DEC-2003; 2003US-00724972.
                   Staphylococcus epidermidis.
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Best Local Similarity 93.5%;
Matches 261; Conservative
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                                                                                                                                                                                                                                                  DOUCETTE-STAMM
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                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADS03304.
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                                                       US2004147734-A1.
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                                                                                                                                                                     08-NOV-1997;
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                                                                                                                                                                                                             29-NOV-1999;
                                                                                                                                                                                                                                                                    BUSH
                                                                                            29-JUL-2004
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181 GEVRMILSTCRATIGQVGNLQHELVNVGKAGRSRWKGVRPTVRGSVMNPNDHPHGGGGGR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for treating or preventing staphylococcal infections or colonisation against S. aureus or S. epidermidis. The antibody preparations may also be used for diagnostic and imaging purposes. Other conditions that can be treated include cancer, autoimmune diseases or infections caused by viral (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This sequence represents a staphylococcal protein relating to the method for identifying and producing pathogen specific antigens of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pathogen specific antigen related staphylococcal protein SEQ ID No 271.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zauner W;
Hafner M;
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, Weichhart T,
                                                                                                                                                                                    241 APIGRPSPWSPWGKPTLGKKTRRGKKSSDKLIVRGRKKK 279
                                                                                                                                       241 APIGRPSPMSPWGKPTLGKKTRRGKKSSDKLIVRGRKKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Von Ahsen U, Klade C
O, Etz H, Dryla A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABJ19022 standard; protein; 277 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune disease; HIV; hepatitis.
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us-09-839-695b-13.rag

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proliferation of the activity of a gene in an inception required to proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for each of the proliferation to to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                        the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for
invention relates to an isolated nucleic acid comprising any one of 6213 antisense seminances river in the comprise of
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Sequence 277 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 GEVRMILSTCRATIGQVGNLQHELVNVGKAGRSRWKGIRPTVRGSVMNPNDHPHGGGEGR 238
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                                                                                                   1 MAIKKYKPITNGRRNMTSLDFAEITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
                                                                                                                               1 MALKKYYPITNGRRNWTSLDPAEITKSTPEKSLLQPLPKKAGRNNQGKLTVRHHGGGHKR
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                                                     Gaps
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Query Match 94.8%; Score 1380; DB 6; Length 277; Best Local Similarity 94.3%; Pred. No. 1.1e-129; Matches 263; Conservative 11; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 APIGRPSPMSPWGKPTLGKKTRRGKKSSDKLIVRGRKKK 279
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Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
                                                                                                 Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3260.
                        ABP38415 standard; protein; 279 AA.
                                                                         (first entry)
                                                                         24-JUL-2002
                                                ABP38415;
RESULT 9
              ABP38415
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Staphylococcus epidermidis

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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 MALKKYKPITNGRRNWTTLDFAEITKTTPEKSLLQPLPKRAGRNNQGKLTVRHHGGGHKR
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                                                                                                                                                                                                                                                                Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
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                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 3260; 267pp; English
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                                                                                                                                                       (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                        97US-0055779P.
                                                                           98US-00134001
                                                                                                                                                                                       Noucette-Stamm LA, Bush D;
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N-PSDB; ABN90960.
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                                                                           13-AUG-1998;
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                US6380370-B1
                                             30-APR-2002
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Local Similarity
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                                                               Sequence 277
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Wall D,
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the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formet directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused S. aureus, e.g. sepsis.
                                                                                                                                                                         QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKR--YIIAPKGLEVGQIVES
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                                                                                              Gaps
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                                                                         DB 6; Length 277;
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                                                                        Query Match 97.0%; Score 1412; DB 6; Best Local Similarity 98.2%; Pred. No. 6.9e-133; Matches 274; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 4358; 49pp; English.
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                                                                                                                                                                                                                                                                                                                                                                 ABM72939 standard; protein;
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N-PSDB; ACF74499.
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                                                    Sequence 277 AA;
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infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
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Xu HH;
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Forsyth I
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Pred. No. 6.9e-133;
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Yamamoto R,
                                                                                                                                                                                                                                                          1; Mismatches
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                         97.0%;
98.2%;
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Trawick JD,
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Identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises providing antibody
                    Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV; hyperimunus; serum-raeactive; antigen; pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer; autoimmune disease; HIV; hepatitis.
Pathogen specific antigen related staphylococcal protein SEQ ID No 222.
                                                                                                                                                                                                                   Zauner W;
Hafner M;
                                                                                                                                                                                                                  Von Ahsen U, Klade C, Henics T,
O, Etz H, Dryla A, Weichhart T,
                                                                                                                                                                                              (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
                                                                                                                                                                                                                                                                                                                                               Example 7; Page 186; 252pp; English
                                                                                                                                                21-JAN-2002; 2002WO-EP000546
                                                                                                                                                                       26-JAN-2001; 2001AT-00000130
                                                                                                                                                                                                                  Meinke A, Nagy E, Von
Minh DB, Vytvytska O,
Tempelmaier B;
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                                                                             Staphylococcus sp.
                                                                                                   WO200259148-A2
                                                                                                                          01-AUG-2002
                                                                                                                                                                                                                                                                                                                         preparation
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The invention relates to a novel method for identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, tumour, allergen, a tissue or host prone to auto-immunity, where the antigens are used in a vaccine, comprises providing antibody preparation from a plasma pool of a type of animal, or individual sera with antibodies against the specific pathogen, tumour, allergen, tissue or host prone to auto-immunity. The hyperimmune serum-reactive antigens comprising any of the 62 sequences of 53-261 amino acids fully defined in the specification, or their hyperimmune fragments are useful for the manufacture of a pharmaceutical preparation, particularly a vaccine against staphylococcal infections or coloniaation against S. aureus or S. epidermidis. The preparation of antibodies is useful for the manufacture of a medicament for treating or preventing staphylococcal infections or coloniaation against S. aureus or S. epidermidis. The antibody preparations may also be used for diagnostic and imaging purposes. Other conditions that can be treated include cancer, autoimmune diseases or infections caused by viral (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This sequence represents a staphylococcal protein relating to the method for sequence represents a staphylococcal protein relating to the method for identifying and producing pathogen specific antigens of the invention

or screening

New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 43760; 1766pp; English.

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Zamudio C, Trawick JD,

υŗ Wang | WPI; 2003-029926/02 N-PSDB; ACA19706.

Sequence 277 AA;

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1;
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                                                                                                                                              180
                                                                                                                                                                                                         119 GARADIKVGNALPLONIPVGTVVHNIELKPGKGGQIARSAGASAQVLGKBGKYVLIRLRS 178
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                                                                                              1 MAIKKYKPITNGRRNMTSLDFAEITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
                                                                                                                                                                                         GAEADTKVGNALPLQNI PVGTVVHNI ELKPGKGGQIARSAGASAQVLGKEGKYVLIRLRS
                                                              1 MAIKKYKPITNGRRNMTSLDPABITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
                                                                                                                               OYRVI DFKRNKDGI NAKVDSI QYDPNRSANI ALVVYADGEKRI YHCI APKGLEVGQI VES
                                   2; Gaps
Score 1412; DB 6; Length 277;
Pred. No. 6.9e-133;
1; Mismatches 2; Indels
      97.0%;
98.2%;
    Query Match 97.0
Best Local Similarity 98.2
Matches 274; Conservative
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Antisense; prokaryotic essential gene; cell proliferation; drug design
      239 APIGRPSPMSPWGKPTLGKKTRRGKKSSDKLIVRGRKKK 277
                                                                                  Protein encoded by Prokaryotic essential gene #1363.
241 APIGRPSPMSFWGKPTLGKKTRRGKKSSDKLIVRGRKKK
                                            Ź
                                            ABU15836 standard; protein; 277
                                                                                                                                                                     06-SEP-2001; 2001US-00948993.
25-007-2001; 2001US-0342923P.
08-FEB-2002; 2002US-036289P.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                   21-MAR-2002; 2002WO-US009107
                                                                                                                                                                21-MAR-2001; 2001US-00815242.
                                                                     19-JUN-2003 (first entry)
                                                                                                                                                                                                       (ELIT-) ELITRA PHARM INC.
                                                                                                            Staphylococcus aureus
                                                                                                                         WO200277183-A2
                                                                                                                                       03-OCT-2002.
                                                         ABU15836;
                               RESULT 6
                                      ABU1583(
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The invention relates to an isolated nucleic acid comprising any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid nucleic acid, (2) a host cell containing the vector; (3) an isolated contacted acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) inhibiting cellular proliferation or the activity of agene in an operon required for proliferation or the activity of agene in an operon required for proliferation, (7) identifying a compound that influences the activity of identifying a gene required for cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the extent or organism orts; (9) manufacturing an antibiotic; (10) profiling a product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for dentifying proteins or screening for homologous nucleic acids required for collection of an organism. The antisense nucleic acids are useful for dentifying proteins or screening for homologous nucleic acids required for collection of an organism. The antisense modeled acids are useful for all antisense modeled and acids and actional action of an organism. drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of

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N-PSDB; AAS52071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 277 AA;
            23-OCT-2000; 27-NOV-2000; 22-DEC-2000;
                                                                                                                    Haselbeck R,
Yamamoto RT,
26-MAY-2000;
                                                         16-FEB-2001;
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                                                    The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The used to screen compounds in rational drug discovery programmes. The used to screen compounds in rational drug discovery programmes. The used to screen compounds in rational drug discovery programmes. The nutisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in clecturic format directly from WiPo at
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                                                                                                                                                                                                                                                                                                                                                                       97.0%; Score 1412; DB 4; Length 277; 98.2%; Pred. No. 6.9e-133; ive 1; Mismatches 2; Indels 2
antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus cellular proliferation protein #488.
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                           Example 3; SEQ ID NO 12767; 511pp; English.
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23-MAY-2000; 2000US-0206848P
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antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 98.2
Matches 274; Conservative
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                                                                                                                                                                                                                                                                                                                                              Sequence 277 AA;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes, themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to expressed proteins. The proteins can antisense nucleic acids sequence is also useful to screen for homologous nutlescense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed sequences.
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                                                                                                                                                                                                                                                         Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APIGRPSPMSFWGKPTLGKKTRRGKKSSDKLIVRGRKKK 277
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2000US-0242578P.
2000US-0253625P.
2000US-0257931P.
2001US-0269308P.
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                                                                                                                                                                                                                                                  Ohlsen KL,
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 98.2
Matches 274; Conservative
                                                                                                                                                                                     (ELIT-) ELITRA PHARM INC
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RESULT 3
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                                                                                                                                                                                  238
                                          120
                                                                                               121 GARADTKVGNALPLQNIPVGTVVHNIELKPGKGGQIARSAGASAQVLGKEGKYVLIRLRS 180
                9
                                                          61 QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKR--YIIAPKGLEVGQIVES
119 GAEADIKVGNALPLQNIPVGTVVHNIELKPGKGGQIARSAGASAQVLGKEGKYVLIRLRS
                                                                                                                                                                         QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVES
                                                                                                                                                       181 GEVRMILSTCRATIGQVGNLQHELVNVGKAGRSRWKGIRPTVRGSVMNPNDHPHGGGEGR
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                                                                                                                                                                                                                                                                                                                AAU36656 standard; protein; 277 AA
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26-WAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-024278P.
27-WOY-2000; 2000US-0253655P.
22-DEC-2000; 2000US-0257931P.
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                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus
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N-PSDB; AAS54515.
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                       14-FEB-2002
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antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                      180
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                                                                                                                                                                                                                                                                                                                                   61 QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKR--YIIAPKGLEVGQIVES
                                                                                                                                                                                                                                        1 MAIKKYKPITNGRRNMTSLDFABITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
                                                                                                                                                                                                                                                                                                                                                                                        GAEADTKVGNALPLQNIPVGTVVHNIBLKPGKGGQIARSAGASAQVLGKEGKYVLIRLRS
                                                                                                                                                                                                                                                                                                                                                                                                                      119 GAEADIKVGNALPLQNIPVGTVVHNIELKPGKGGQIARSAGASAQVLGKEGKYVLIRLRS
                                                                                                                                                                                                                                                              1 MAIKKYKPITNGRRNMTSLDFAEITKTTPEKSLLKPLPKKAGRNNQGKLTVRHGGGHKR
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                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense; prokaryotic cellular proliferation protein; antibiotic;
                                                                                                                                                                                                         2;
                                                                                                                                                                          Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus cellular proliferation protein #1344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides for the identification and development
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 APIGRPSPMSPWGKPTLGKKTRRGKKSSDKLIVRGRKKK 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 APIGRPSPMSPWGKPTLGKKTRRGKKSSDKLIVRGRKKK 279
                                                                                                                                                                        97.0%; Score 1412; DB 4;
98.2%; Pred. No. 6.9e-133;
iive 1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU37174 standard; protein; 277 AA
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26-MAY-2000; 2000US-020727P.
23-OCY-2000; 2000US-0242578P.
22-DEC-2000; 2000US-0253625P.
16-FEB-2001; 2001US-025931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibacterial; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-FEB-2002 (first entry)
                                                                                                                                                                                           Best Local Similarity 98.2
Matches 274; Conservative
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                                                                                                                                          Sequence 277 AA;
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Yamamoto RT,
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Streptoco

Protein

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Novel S.

Abp28607 Adk47631 Adr95979 Adb06496 Ads29482

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1 MAIKKYKPITNGRRNMTSLDFAEITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
                                                      ADR95979
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                                                                                                                                                                                                                                                                                                                                                                   AAY70416 standard; protein;
 Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                        hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                   - protein search, using sw model
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ABU14500
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AAU33423
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geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
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geneseqp2003as:*
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                                                                                                                                                                                                        BLOSUM62
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Match
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antibacterial agent; treatment; prevention; bacterial infection.
                                                                                                                                                                                                                                                                      Protein e
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                                                                              Alloiococ
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                                                                                                                                                                                                                                                    Bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Staphylococcus aureus polypeptides used for isolating antibacterial agent for treating bacterial infections.
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                                   Abb55450
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Adb06494
Abu23813
Abu24460
Abu25097
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Adn26212
Abu48842
Ads30785
Ads44982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus ribosomal protein RPL2.
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ADB06496
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119

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Gaps

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Query Match

238 EGRAPIGRPSPMSPWGKPTLGKKTRRGKKSSDKLIVRGRKK 278

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1 MAVKRIKUHSSGKRQTVVVDYKSILTTSKPEKSLLVTLPKKAGRNNQGKITIRHHGGGHK
                                                                                                                                                                                                                   60 RQYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                              177 RLRSGEVRMILSTCRATIGQVGNLQHELVNVGKAGRSRWKGIRPTVRGSVMNPNDHPHGG
                                                                                                           1 MAIKKYKPITNGRRNMTSLDFAEI-TKTTPEKSLLKPLPKKAGRNNOGKLTVRHHGGGHK
, Score 895, DB 2; Length 279;
, Pred. No. 2.1e-63;
40; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 GEGRSPVGMDAPRTPWGKRHMGVKTRNNKKSSTSMIVRRKK 279
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     62.3%;
                              Best Local Similarity 62.3
Matches 175; Conservative
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min; Reference number: A82870
Accession: G82915
Accession: G82915
Beatus: preliminary
Molecule type: DNA
Residues: 1-79 cGLAB
CROSs-references: GB:AE002123; GB:AF222894; NID:g6899229; PIDN:AAF30643.1; GSPDB:GN001; Experimental source: servovar 3; biovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:QBYP12; GB:BA000019; PIDN:BAB75911.1; PID:g17133347; GSPDB:G
A;Experimental source: strain PCC 7120
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R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000
                                                                                                                                                                                     508 ribosomal protein L2 [imported] - Nostoc sp. (strain PCC 7120)
C.ispecies: Nostoc sp. PCC 7120
A.Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 QYRVIDEKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVES 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEVRMILSTCRATIGQVGNLQHELVNVGKAGRSRWKGIRPTVRGSVMNPNDHPHGGGEGR 240
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C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 07-Jul-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAIKKYKPITNGRRNMTSLDPAEITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
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61.6%; Score 897; DB 2; Length 287;
Best Local Similarity 62.6%; Pred. No. 1.5e-63;
Matches 174; Conservative 35; Mismatches 67; Indels
                                   239 EGKQPIGRKAPLTPWGKKALGVKTRDNKKSSTKLIIRRRKE 279
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Superfamily: ribosomal protein L2/L8
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A;Molecule type: DNA
A;Residues: 1-287 <KUR>
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A;Residues: 1-6,'N',8-18,'TECSLFNNQKIA',31-35,'GG',38-41,'TA',44-46,'KS',49-51,'SS',54-28
C;Genetics:
A;Genetic code: SGC3
A;Genetic code: SGC3
C;Superfamily: ribosomal protein L2/L8
C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOS ribosomal protein L2 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Accession: A99585
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis A;Reference number: A99512; MuID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-281 <KUR>
A;Cross-references: UNIPROT:Q98PY4; GB:AL445566; PID:g14090000; PIDN:CAC13758.1; GSPDB:GN
A;Experimental source: strain UAB CTIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 RLRSGEVRMILSTCRATIGQVGNLQHELVNVGKAGRSRWKGIRPTVRGSVMNPNDHPHGG 236
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                                                                                                                                                                           65.8%; Score 958; DB 1; Length 281;
65.0%; Pred. No. 2.2e-68;
iive 40; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 GEGRAPIGRPSPMSPWGKPTLGKKTRRGKKSSDKLIVRGRKKK 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: MYPU 5850
A;Genetic code: SGC3
C;Superfamily: ribosomal protein L2/L8
                                                                                                                                                                                                     Best Local Siminarity v.v. Matches 184; Conservative
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A, Molecule type: DNA
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                                                                                                                                                                                                                                                                    Tibosomal protein L2 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97285
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld A;Reference number: A96900; MUD:21359325; PMID:21359325
A;Reference number: A96900; MUD:21359325; PMID:21359325
A;Residues: PORA
A;Molecule type: DNA
A;Residues: 1-277 < KUR>
A;Residues: 1-277 < KUR>
A;Residues: 1-277 < KUR>
A;Cross-reference: UNIPROT:097EII; GB:AE001437; PIDN:AAK81069.1; PID:g15026196; GSPDB:G
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                          1 MAIKKYKPITNGRRNMTSLDFAEITKTTPEKSLLKPLPKKAGRNNOGKLTVRHHGGGHKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVES
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                                                                                                                              239 APIGRKSPMTPWGKKARGVKTRDRKKASNALIIRRRTK 276
                                                                                                    241 APIGRPSPMSPWGKPTLGKKTRRGKKSSDKLIVRGRKK 278
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A;Reference number: 805072
A;Accession: 805072
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A, Molecule type: DNA
A, Residues: 1-281 - OHK>
A, Cross-references: UNIPROT:P10133; EMBL:X06414
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C,Superfamily: ribosomal protein L2/L8
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C;Accession: B54547
R;Lim, P.O.; Sears, B.B.
FEMS Microbiol. Lett. 68, 71-73, 1991
A;Title: DNA sequence of the ribosomal protein genes rp12 and rps19 from a plant-pathoger A;Reference number: A54547; MUID:92120503; PMID:1769558
A;Reference number: A545477
                                                          A,Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssg
A,Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                GB:AE005176; PID:g12725150; PIDN:AAK06194.1; GSPDB:GN
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R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach,
Genome Res. 11, 731-753, 2001
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C;Species: mycoplasma-like organisms, MLOs
C;Date: 06-Oct-1994 #sequence_revision 25-Apr-1997 #text_change 07-Jul-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGIKVYKPTTNGRRNMTGSDFABITTSTPEKSLLVSMSKTAGRNNTGRITVRHHGGGHKR
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A;Note: sequence extracted from NCBI backbone (NCBIN:77580, NCBIP:77582)
C;Superfamily: ribosomal protein L2/L8
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llarity 74.8%; Pred. No. 2.1e-77;
Conservative 24; Mismatches 43;
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Pred. No. 2e-69;
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                                                                                                                                                                                                                                                                                                                                                                     A;Gene: rplB
C;Superfamily: ribosomal protein L2/L8
                                                                                                                                                                                                                          A,Residues: 1-276 <STO>
A,Cross-references: UNIPROT:Q9CDW5; CASExperimental source: strain IL1403
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68.0%;
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Best Local Similarity 68.0%
Matches 189; Conservative
                                      Genome Res. 11, 731-753, A; Title: The complete gen
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Matches 205; Conserv
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                                                                                                                                   A; Accession: H86886
A; Status: preliminary
A; Molecule type: DNA
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. Accession: G97895
R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; F. R.; Leeb L.D., J. Leeb L.D., J. Leeb L.D.; Leeb L.D.;
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50S ribosomal protein L2 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          508 ribosomal protein L2 [imported] - Streptococcus pneumoniae (strain R6) C;Species: Streptococcus pneumoniae C;Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
                                                                                                    61 QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVES
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1 MAIKKYKPITNGRRNMTSLDFABITKTTPBKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
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A;Experimental source: strain TIGR4
C;Genetics:
R;Kroemer, W.J.; Hatakeyama, T.; Kimura, M.
Bol. Chem. Hoppe-Seyler 371, 631-636, 1990
A;Title: Nucleotide sequences of Bacillus stearothermophilus ribosomal protein genes: par A;Reference number: S10610; MUID:91025633; PMID:2222862
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C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: G95024
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.B.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 EVRMILGKCRATVGEVGNEQHELVNIGKAGRARMLGIRPTVRGSVMNPVDHPHGGGEGKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 275;
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75.3%; Pred. No. 3e-80;
tive 26; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.3%; Score 1125; DB 1;
75.8%; Pred. No. 1.3e-81;
tive 30; Mismatches 35;
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C,Superfamily: ribosomal protein L2/L8
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Best Local Similarity 75.8%
Matches 210; Conservative
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Best Local Similarity 75.39
Matches 210; Conservative
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A;Molecule type: DNA
A;Residues: 1-277 <KUR>
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C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A02759; S10610; S5908
R;Kimura, M.; Kimura, J.; Watanabe, K.
Eur. J. Biochem. 153, 289-297, 1985
A;Title: The primary structure of ribosomal protein L2 from Bacillus stearothermophilus. A;Reference number: A02759; MUID:86081765; PMID:3908098
                                                                                                                                                                                                                                                                         C;Species: Bacillus halodurans
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C;Date: 31-Jan-3000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
R;Takami, H.; Takaki, Y.; Nakasone, K.; Hirama, C.; Inoue, A.; Horikoshi, K.
Biosci. Biotechnol. Blochem. 63, 452-455, 1999
A;Title: Sequence analysis of a 32-kb region including the major ribosomal protein gene A;Accession: T44386
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A,Experimental source: strain C-125
A,Experimental source: strain C-125
A,Flakani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Adids Res. 28, 4317-4331, 2000
A,Title: Complete genome sequence of the alkaliphilic bacterium Bacillus haloduxans and
A,Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BAB03856.1; GSPDB:GN00
A;Experimental source: strain C-125
                                                                                                                                                                                                                                               ribosomal protein L2 (BL2) rplB [imported] - Bacillus halodurans (strain C-125)
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241 APIGRPSPMSPWGKPTLGKKTRRGKKSSDKLIVRGRKK 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-276 <TAK>
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RSBS2F
ribosomal protein L2 - Bacillus stearothermophilus
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C;Superfamily: ribosomal protein L2/L8
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A;Residues: 1-275 <KIM>
A;Cross-references: UNIPROT:P04257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Accession: A8367
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-276 <STO>
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C; Accession: F69694

B; Kunst, F; Ogasawara, N.; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V.; Bertere C; Accession: F69694

B; Kunst, F; Ogasawara, N.; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V.; Bertere C; Ebron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E. A,Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallere A,Authors: Poller, D.; Fritz, C.; Fujita, M.; Fujita, M.; Fuma, S.; Galizzi, A.; Gallere X,Authors: Laber, D.; Korlngstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Laudinois, A,Authors: Laber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelle, R.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Scanon, A.; Saco, T.; Scanon, A.; Muthors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Saco, Y.; Scanon, T.; Winters, P.; Wipat, A.; Tanaka, T.; Terpetra, P.; Tognonl, A.; Tosato, V.; Uchiyama, H.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yata, C.; Voshida, K.; Matelerence number: A; Reference equence equence of the Gram-positive bacterium Bacillus subtilis.
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A;Molecule type: DNA
A;Residues: 1-277 <KUN>
A;Cross-references: UNIPROT:P42919; GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CAB11895.1
                                                                                                                                                                                                                                                                                                                      121 GAEADTKVGNALPLQNIPVGTVVHNIELKPGKGGQIARSAGASAQVLGKEGKYVLIRLRS 180
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
61 QYRVIDFKRNKDGIPGRVATIEYDFNRSANIALINYADGEKR--YIIAAKGLEVGQTIYS
                                                                                                                                                                                                                                                                                                                                                                         119 GAEADIKVGNALELKDIPVGTVIHNIEMKPGKGGQLVRSAGTSAQVLGKEGKYVLIRLNS
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                                                                                                                                        61 QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEVRMILSTCRATIGOVGNLQHELVNVGKAGRSRWKGIRPTVRGSVMNPNDHPHGGGEGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: F69694
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1779
C;Accession: AD179
C;Baser, D: Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
S;Jaser, P: Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Bartian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-8552, 201
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Sc
                                     Riciaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
A,Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A,Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A,Theis: Comparative genomics of Listeria species.
A,Reference number: AB1077; MUID:21537279; PMID:11679669
A,Accession: AE1403
A,Accession: AE140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: UNIPROT:P60425; GB:AL592022; PIDN:CAC98004.1; PID:g16415314; GSPDB:G;
Experimental source: strain Clip11262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 GEVRMILSTCRATIGQVGNLQHELVNVGKAGRSRWKGIRPTVRGSVMNPNDHPHGGGEGR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61. QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 82.6%; Score 1203; DB 2; Best Local Similarity 82.4%; Pred. No. 9.1e-88; Matches 230; Conservative 20; Mismatches 27;
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-277 < GLA>
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

June 9, 2005, 15:57:59 ; Search time 40 Seconds (without alignments) 671.112 Million cell updates/sec Run on:

US-09-839-695B-13 1456 1 MAIKKYKPITNGRRNMTSLD......KTRRGKKSSDKLIVRGRKKK 279 Title: Perfect score: Sequence:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | 1 | Description | Q | _ | ribosomal protein | | | ribosomal protein | ribosomal protein | 50S ribosomal prot | О | prot | | ribosomal protein | 50S ribosomal prot | 50S ribosomal prot | | _ | н | _ | | ribosomal protein | О | | | ribosomal protein | 50S ribosomal prot | ribosomal protein | 50S ribosomal prot | | ribosomal protein |
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| | 4 | a i | B90022 | AE1403 | AD1779 | F69694 | T44386 | R5BS2F | G95024 | G97895 | H86886 | B54547 | B97285 | R5YM2C | A99585 | AE2332 | C82915 | B75534 | C70642 | C82059 | A72250 | R5EB2Y | AE0026 | R5KT2 | T45367 | S78273 | D82005 | S77499 | C81231 | B83116 | R5EC2 |
| | 1 | 80 : | N | ~ | ~ | ~ | ~ | Н | 7 | ~ | 7 | 7 | 7 | ٦ | N | 7 | 7 | 7 | 7 | 7 | ~ | н | 7 | | 7 | ~ | 7 | 7 | ~ | ~ | Н |
| | • | Match Length | 277 | 277 | 277 | 277 | 276 | 275 | 277 | 277 | 276 | 276 | 277 | 281 | 281 | 287 | 279 | 275 | 280 | 274 | 276 | 274 | 274 | 275 | 280 | 275 | 277 | 276 | 277 | 273 | 273 |
| | Query | ch | 0.7 | 9.2 | 9.2 | 6. | 6.3 | 7.3 | 5.1 | 1.94 | 3.6 | 5.7 | 9.6 | 65.8 | 3.2 | 1.6 | 1.5 | 8.0 | 0.4 | 2. | 6.0 | 2.5 | 9.2 | 7.8 | 7.8 | | 7.9 | 7.8 | 7 | | 7.5 |
| æ | ð: | Ma | è | æ | 82 | 79 | 79 | 7 | 16 | ~ | 7 | Ğ | ō | Ö | Ġ | Ö | 61 | 9 | ō | ō | ŭ | 'n | Ŋ | ñ | 58 | Ñ | 'n | Ņ | 'n | 'n | 'n |
| | • | Score | 1412 | 1203 | 1203 | 1163 | 1154 | 1125 | 1108 | 1108 | 1072 | 971 | 696 | 958 | 920.5 | 897 | 895 | 882 | 880 | 876 | 871.5 | 862.5 | 862.5 | 855 | 855 | 846 | 843 | 842 | 842 | 838 | 837.5 |
| | Result | No. | - | 7 | ٣ | 4 | 2 | 9 | 7 | 80 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 29 |

| 50S ribosomal subu | | 50S ribosomal chai | ribosomal protein | 50S ribosomal prot | 50S ribosomal prot | ribosomal protein | ribosomal protein | 50S ribosomal prot | ribosomal protein | ribosomal protein | ribosomal protein | ribosomal protein | probable ribosomal | ribosomal protein | LSU ribosomal prot |
|--------------------|---------|--------------------|-------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|--------------------|
| B85997 | 791151 | 4D1006 | H64092 | F84990 | D81268 | S26081 | H70159 | C82717 | 873232 | T07361 | A64217 | R5LV2 | B71355 | 873989 | AB3347 |
| | - | - | | | | | | | | | | | | | |
| 7 | 7 | 7 | 7 | ~ | 0 | N | ~ | ~ | ~ | N | N | П | ~ | ~ | ~ |
| 273 2 | 273 2 F | 7 | 273 2 | 273 2 | 276 2 | 277 2 | 277 2 | 275 2 | 294 2 | 275 2 | 285 2 | 277 1 | 273 2 | 287 2 | 277 2 |
| | N | 273 2 | | | | | | | | | | | | | |
| 57.5 | 273 2 | 57.5 273 2 | 57.3 | 9.99 | 56.3 | 26.0 | 55.9 | 55.8 | 55.7 | 55.4 | 55.4 | 54.0 | 53.7 | 53.6 | 53.2 |

ALIGNMENTS

| | RESULT 1 B90022 508 ribosomal | RESULT 1 B90022 508 ribesomal protein L2 [imported] - Staphylococcus aureus (strain N315) C.Sneries: Stanhylococcus aureus |
|---|---|---|
| | C;Date: 10-May-2001 | C.becies: 10-34/2011 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 |
| | R; Kuroda, M.; ma, A.; Mizut | Cincotesion: Syoua, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch R.; Kuroda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Fama, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, D.; Sekimizu, K.; Fama, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, D.; Sekimizu, K.; Fama, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, D.; Sekimizu, K.; Fama, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Sawano, T.; Sekimizu, K.; Fama, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Sawano, T.; Sawano, T.; Sekimizu, K.; Fama, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; |
| | Lancet 357, 1 | C.; Shila, I.; hattori, m.; Ogabawara, M.; nayabii, m.; hiramatsu, M. Lancet 357, 1225-1240, 2001 |
| | A;Title: Whol A;Reference n | A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 |
| | A, Accession: B90022 | 890022 |
| | A;Status: preiiminary A;Molecule type: DNA | Limitary pe: DNA |
| | A; Residues: 1-277 <kur></kur> | -277 «KUR» |
| | A; Cross-refer | A; Cross-references: UNIPROT: F60422; GB: BA000018; PID: 913702047; PIDN: BAB4339.1; GSPDB: GP |
| | A; Experimenta C; Genetics: | Ajazgerimentai source: Burain Nais Cjemetics: |
| | A;Gene: rplB C;Superfamily | A;Gene: rplB C;Superfamily: ribosomal protein L2/L8 |
| - | doteM Watch | 97 0%: Score 1412: DB 2: Length 277: |
| | Best Local Similarity Matches 274; Conser | 98.2%; Pred. No. 2.7e-104; vative 1; Mismatches 2; |
| | ģ | 1 MAIKKYKPITNGRRNMTSLDFABITKTTPBKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR 60 |
| | d 1 | |
| | Qy 61 | OYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVES 120 |
| | Db 61 | |
| | Qy 121 | GAEADTKVGNALPLONI PVGTVVHNI ELKPGKGGQI ARSAGASAQVLGKEGKYVLIRLRS 180 |
| | 011 da | GAEADIKVGNALPLQNIPVGTVVHNIELKPGKGGGIARSAGASAQVLGKEGKYVLIRLRS 178 |
| | Qy 181 | GEVRMILSTCRATIGOVGNLQHELVNVGKAGRSRWKGIRPTVRGSVMNPNDHPHGGGGGR 240 |
| | 179 da | GEVRMILSTCRATIGOVGNLQHELVNVGKAGRSRWKGIRPTVRGSVMNPNDHPHGGGEGR 238 |

8 8

RESULT 2
AE1403
ribosomal protein L2 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

Search completed: June 9, 2005, 16:07:21 Job time : 176 secs

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STRAIN=Sterne;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 QYRIIDFKRNKDGIPGRVATIEYDPNRSANIALINYVDGEKR--YILAPKGLKVGWTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GAEADTKVGNALPLQNIPVGTVVHNIELKPGKGGQIARSAGASAQVLGKEGKYVLIRLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 GPEADIKVGNALPLKNIPVGTVIHNIELKPGKGGQLVRSAGAEAQLLGKBGYVLVRLNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEVRMILSTCRATIGQVGNLQHELVNVGKAGRSRWKGIRPTVRGSVRNPNDHPHGGGGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 GETRYILATCRATIGOVGNLEHELVNIGKAGRSRWLGKRPTVRGSAMNPNDHPHGGGEGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T., Nelson K.E., Tettelin H., Fouts D.B., Eisen J.A., Gill S.R., Holtzapple B.K., Okstad O.A., Helgason B., Rilstone J., Wu M., Kolonay J. P., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L., Nelson W.C., Peterson J.D., Popp M., Knouri H.M., Radne D.H., Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman W.C., Hazen A., Cline R.T., Redmond C., Thwaite J.E., Nierman W.C., Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O., Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                        R PIR; T44386; T44386.

R HSSP; P04257; IRL2.

R HAMAP; MF 01320; -; 1.

R InterPro; IPR008994; Nucleic acid OB.

R InterPro; IPR008994; Nucleic acid OB.

R InterPro; IPR008991; Transl L2 b/o.

R InterPro; IPR008991; Transl L2 b/o.

R Pfam; PF00181; Ribosomal L2; 1.

R Pfam; PF0181; PS00467; RIBOSOMAL L2; 1.

R PROSITE; PS00467; RIBOSOMAL L2; 1.

COMPLETE proteome; Ribosomal protein; RNA-binding; rRNA-binding.

COMPLETE 276 AA; 30224 MW; ABD31A20D6479696 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.3%; Score 1154; DB 1; Length 276; 78.4%; Pred. No. 2.9e-82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RL2 BACAN STANDARD; PRT; 276 AA. 0818/27; 061471; 06KYH7; 29-MAR-2004 (Rel. 43, Created) 29-MAR-2004 (Rel. 43, Last sequence update) 25-0CT-2004 (Rel. 45, Last annotation update) 50S ribosomal protein L2. Name=rplB; OrderediocusNames=BA0113, GBAA0113, BAS0113; Bacillus anthracis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 APIGRKSPMSPWGKPTLGYKTRKKNKASDKYIVRRRKK 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Mismatches
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STRAIN-Ames / isolate Porton;
EMBL; AP001507; BAB03856.1;
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STRAIN=Ames / isolate 0581;
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Matches 218; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                  Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin B., Tice H., Submitted (JAN 2004) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: One of the primary rRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for tRNA binding and peptide bond formation. It has been suggested to have peptidyltransferase activity; this is somewhat controversial. Makes several contacts with the 16S rRNA in the 70S
Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B., Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L., Fraser C.M.; Bacillus anthracis comparative genomics."; Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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SuBONIT: Part of the 508 ribosomal subunit. Forms a bridge 308 subunit in the 708 ribosome (By similarity).
SIMILARITY: Belongs to the ribosomal protein L2P family.
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HSSP; PO4213; -.
TIGR; BA0113; -.
TIGR; GBA0113; -.
TIGR; GBA0113; -.
HAMAP; MF 01320; -; 1.
HAMAP; MF 01320; -; 1.
HAMAP; MF 01309; -; 1.
HAMAP; MF 01008994; Nucleic acid OB.
InterPro; IPR008991; Ribosomal_L2 bo.
InterPro; IPR00891; Trans1_SH3_lke.
FEan; PP00181; Ribosomal_L2; 1.
FEan; PP03947; Ribosomal_L2; 1.
FEan; PS03467; Ribosomal_L2; 1.
TIGRFAMS; TIGR0111; TplB_Dact; 1.
FOSTIF: PS00467; Ribosomal_Drotein; RNA-binding; FRNA-bi SEQUENCE 276 AA; 30253 MW; FE3202D9F88FDE90 CRC64;
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                                                    119 PEADIKVGNALPLINIPVGTVVHNIELKPGKGGQLVRSAGTSAQVLGKEGKYVLVRLNSG 178
                                                                                                                                                                              241
                                                                                                                                                                                                 YRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVESG 121
                                                                                                     122 AEADTKVGNALPLONIPVGTVVHNIELKPGKGGQIARSAGASAQVLGKEGKYVLIRLRSG 181
1 AIKKYKPSSNGRRGMTTSDPAEITTDKPEKSLLAPLHKKGGRNNOGKLTVRHOGGGHKRO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 30:3927-3935(2002).
-!- FUNCTION: One of the primary rRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for tRNA binding and peptide bond formation. It has been suggested to have peptidyltransferase activity; this is somewhat controversial. Makes several contacts with the 16S rRNA in the 70S
                                                                                                                                                                              EVRMILSTCRATIGQVGNLQHELVNVGKAGRSRWKGIRPTVRGSVMNPNDHPHGGGEGRA
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R HANAP; MF 01320; -; 1.

R INTERPRO; IPR008994; Nucleic acid OB.

R INTERPRO; IPR008994; Nucleic acid OB.

R INTERPRO; IPR008991; Ribosomal L2.

DR INTERPRO; IPR008991; Ribosomal L2; 1.

DR PÉan; PF00181; Ribosomal L2; 1.

DR PÉan; PF03947; Ribosomal L2; 1.

DR PROSITE; PS00467; RIBOSOMAL L2; 1.

R PROSITE; PS00467; RIBOSOMAL L2; 1.

KW Complete proteome; Ribosomal protein; RNA-binding; FRNA-binding.

Annumar 276 AA; 30386 MW; C9E65EF0670F9CA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526; Takami H., Takaki Y., Uchiyama I.; "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oceanobacillus ineyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
NCBI_TaxID=182710;
                                                                                                                                                                                                                                                 242 PIGRPSPMSPWGKPTLGKKTRRGKKSSDKLIVRGRKKK 279
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                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-2004 (Rel. 43, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
50S ribosomal protein L2.
Name=rplB; OrderedLocusNames-OB0122;
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STRAIN=HTE831 / DSM 14371 / JCM 11309
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Q8ETX9;
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Well-ground the primary rRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for tRNA binding and peptide bond formation. It has been suggested to have peptidyltransferase activity; this is somewhat controversial. Makes several contacts with the 16S rRNA in the 70S
                                                                                                                                                                                                                                                                                                                                                    179 GEVRLILTTCRATIGOVGNIEHELVRVGKAGRSRWKGIRPTVRGSVMNPNDHPHGGGEGR
                                                                                                                                                      61 QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVES
                                                                                                                                                                              61 QYRIIDFKRDKDG1PGRVATIEYDPNRSANIALVHYADGEKR--YIIAPKG1KVGQEIES
                                                                                                                                                                                                                                                                  119 GENADIKIGNALPLGSIPVGTVIHNIELKPGRGGQIARSAGAEAQILGREEKYTLVRLSS
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SEQUENCE FROM N.A.
STRAINS-1255 / JCM 9153;
MEDLINE-9209008; PubMed=10192928;
Takami H., Takaki Y., Nakasone K., Hirama C., Inoue A., Horikoshi K.;
Takami H., Takaki Y., Nakasone K., Hirama C., Inoue A., Horikoshi K.;
Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic Bacillus sp. strain C-125.";
Biosci. Biotechnol. Biochem. 63:452-455(1999).
                                                                      1 MAIKKYKPITNGRRNMTSLDFAEITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
                                                                                              1 MAIKKFKPISNGRRNMSVSDFAEITIDIPEKSLLSPIRKRGGRNNQGKLTVRHQGGGHKR
                                                                                                                                                                                                                                            GARADIKVGNALPLONI PVGTVVHNI BLKPGKGGQI ARSAGASAQVLGKEGKYVLI RLRS
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                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
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SEQUENCE FROM N.A.
SEQUENCE 125 / JOHN 9153;
MEDLINE=20512583; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
MEDLINE=20512583; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masul N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fuji F., Hirama C., Nakamura Y., Ogasawara N., Ammanan K., Horikoshi K.;
"Complete genome sequence of the alkaliphilic bacterium Bacillus Subtilii
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2e-82;
~hes 31; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                               241 APIGRPSPMSPWGKPTLGKKTRRGKKSSDKLIVRGRKK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                       239 APIGRKSPMSPWGKPTLGYKTRQRNKPSDKYIVRKRKK 276
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Last annotation update)
                            26; Mismatches
           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=rplB; OrderedLocusNames=BH0137;
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30-MAY-2000 (Rel. 39, Last seq
30-MAY-2000 (Rel. 39, Last seq
25-OCT-2004 (Rel. 45, Last and
        78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50S ribosomal protein L2.
                            219; Conservative
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                            Matches
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RL2_BACHD
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2 AIKKYKPITNGRRNMTSLDPAEITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKRQ 61
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                "Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related Bacillus species."; Genome Biol. 5:R77-R77(2004).
EMBL; AE017333; AAU213110.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAIKKYKPISNGRRGMISSDFAEITIDQPEKSLLAPLHKKGGRNNQGKLIVRHQGGGHKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li X., Lindahl L., Sha Y., Zengel J.M.;
"Analysis of the Bacillus subtilis S10 ribosomal protein gene cluster identifies two promoters that may be responsible for transcription of the entire 15-kilobase S10-spc-alpha cluster.";
J. Bacteriol. 179:7046-7054(1997).
                                                                                                                                                                                                                                                                                                   1 MAIKKYKPITNGRRNMTSLDFAEITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
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                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                 Match
Local Similarity 80.3%; Score 1175; DB 2; Length 277;
Local Similarity 80.3%; Pred. No. 6.5e-84;
les 224; Conservative 18; Mismatches 35; Indels 5
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NCBL_TaxID=1423;
                                                                                                                                                             277 AA; 30302 MW; A6B7DDE718836870 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Name=rplB; OrderedLocusNames=BSU01190;
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                                                                                                                                          Ribosomal protein.
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ID RLZ_BACSU
AC P42919;
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Matches
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RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entian K.-D., Erington J., Fabret C., Ferrari E., Foulger D., R. Fritz C., Tujita M., Fujita Y., Funa S., Galizzi A., Galleron N., A. Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Rain C., Kobayashi Y., Koetter P., Koningstein G., Krogh S., Lauber J., Komano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Razarevic C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., R. Parro V., Poll T.M., Portetelle D., Porwollik S., R. Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Ray Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rocffone F., Sadie Y., Sato T., Scanlan E., Schleich S., Schreeter R., Romano M., Tamakoshi A., Taraka T., Terpetra P., A. Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vastumoto K., Yata K., Yoshida K., Yamamoto H., Yamane K., A. Wasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., A. Washille C., Rochi B., Shellech B., Shellech B., Shellech B., Shellech B., Shellech B., Shellech B., Winters P., Wipat A., Yamamoto H., Yamane K., A. Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Tarberium Bacillus T. The Complete genome sequence of the Gram-positive bacterium Bacillus T. The Third B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 390:249-256(1997).

-!- FUNCTION: One of the primary rRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for tRNA binding and peptide bond formation. It has been suggested to have peptidyltransferase activity; this is somewhat controversial. Makes several contacts with the 16S rRNA in the 70S ribosome (By similarity).

-!- SUBDUIT: Part of the 50S ribosomal subunit. Forms a bridge to the 30S subunit in the 70S ribosome (By similarity).

-!- SIMILARITY: Belongs to the ribosomal protein L2P family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35; Indels
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EMBL; D50302; BAA08834.1; -.
EMBL; Z99104; CAB11895.1; -.
PIR, F056594; F69694.
HSSP; P04577; IRL2.
Subtilist; BG11217; rplB.
HAMAP; MF 01320; -; 1.
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Best Local Similarity
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Nucleic Acids Res. 32:2386-2395(2004)
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SEQUENCE FROM N.A.
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                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENED cutstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GAEADTKVGNALPLQNIPVGTVVHNIELKPGKGGQIARSAGASAQVLGKEGKYVLIRLRS 180
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PubMed=15115801; DOI=10.1093/nar/gkh562;
PubMed=15115801; DOI=10.1093/nar/gkh562;
Nelson K.E., Rauko D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,
Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madpup R.,
Haft D.H., Selengut J., van Aken S.E., Khouri H.M., Fedcova N.,
Forberger H.A., Tran B., Kathariou S.E., Wonderling L.D., Uhlich G.A.,
Bayles D.O., Luchansky J.B., Fraser C.M.;
"Whole genome comparisons of sercype 4b and 1/2a strains of the food-
borne pathogen Listeria monocytogenes reveal new insights into the
core genome components of this species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAIKKYKPTINGRRHMISSDFAEITISTPEKSLLRPLKKKAGRNNOGKLIVRHHGGGHKR
                                                                                                                                                                                                                                                                                                                                                                                                             1 MAIKKYKPITNGRRNMTSLDFAEITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
 SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to
                                                                                                                                                                                                                        HAMAP; MF 01320; -; 1.
InterPro; IPR002171; Ribosomal_L2.
InterPro; IPR005880; Ribosomal_L2_b/o.
ITGRPAMS; TIGR01171; rplB_bact; 1.
PROSITE; PS00467; RIBOSOMĀL_L2; 1.
Complete proteome; Ribosomāl protein; RNA-binding; rRNA-binding.
SEQUENCE 277 AA; 30505 MW; DD0D58498AF5A632 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                 82.6%; Score 1203; DB 1; Length 277; 82.4%; Pred. No. 4.2e-86; tive 20; Mismatches 27; Indels
               30S subunit in the 70S ribosome (By similarity).
-!- SIMILARITY: Belongs to the ribosomal protein L2P family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listeria monocytogenes (serotype 4b / strain F2365).
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=265669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 APIGRPSPMSPWGKPTLGKKTRRGKKSSDKLIVRGRKKK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 APIGRKSPMSPMGKPTLGYKTRKKNNNSDKFIVRRRKKK 277
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Name=rplB; OrderedLocusNames=LMOf2365_2602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                               EMBL; AL591983; CAD00707.1; -. PIR; AE1403; AE1403.
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Best Local Similarity
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121 GAEADTKVGNALPLQNIPVGTVVHNIELKPGKGGQIARSAGASAQVLGKEGKYVLIRLRS 180
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Rey M.W., Ramalya P., Nelson B.A., Brody-Karpin S.D., Zaretsky B.J., Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B., Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
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Bhrenzeich P., Bacumer S., Henne A., Liesegang H., Merkl R.,
Bhrenzeich A., Gottechalk G.,
"The Complete Genome Sequence of Bacillus licheniformis DSM13,
R EMBL; AE017331; AACTOSTOCOTO.

R GO; GO:0005622; C:intracellular; IEA.

GO; GO:0003723; F:intacellular; IEA.

GO; GO:0003723; F:intacellular; IEA.

GO; GO:0003725; F:structural constituent of ribosome; IEA.

GO; GO:0003725; F:structural constituent of ribosome; IEA.

GO; GO:0006412; P:procein biosynthesis; IEA.

R GO; GO:0006412; P:procein biosynthesis; IEA.

R InterPro; IPR008994; Nucleic acid OB.

R InterPro; IPR008991; Ribosomal L2.

R InterPro; IPR008991; Trans1 SH3 like.

R Ffam; PF001811; Ribosomal L2.

R Pfam; PF001811; Ribosomal L2.

R Pfam; PF001817; Ribosomal L2.

R PROSITE; PS00467; RIBOSOMAL L2.

Complete proteome; Ribosomal Iprocein.

Complete proteome; Ribosomal Iprocein.

Complete Proteome; Ribosomal Iprocein.
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82.4%; Pred. No. 4.2e-86;
ive 20; Mismatches 27; Indels
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
RplB (Ribosomal protein L2) (BL2).
RplB (Ribosomal protein L2) (BL2).
Bacillus licheniformis DSM 13.
Bacitius licheniformis DSM 13.
RCBL_TAXID=279010;
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Matches 230; Conservative
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SEQUENCE FROM N.A.

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STRAIN=CLIP 11262 / Serovar 6a;

MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;

Glaser P., Frangeul L., Buchrieser C., Rueniok C., Amend A.,

Glaser P., Berche P., Bloecker H., Brandt P., Chakraborty T.,

Andrik A., Chetouani F., Couve B., de Dartvar A., Dehoux P.,

Domann B., Dominquez-Bernal G., Duchaud B., Durant L., Dussurget O.,

Entian K.-D., Fgihi H., Garcia-del Portillo F., Garrido P.,

Butier L., Goobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kunn M., Kunst F., Kurapkat G.,

Madueno B., Maitournam A., Mata Vicente J., Ng B., Nedjari H.,

Nordeiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simose N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

"Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: One of the primary TRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for tRNA binding and peptide bond formation. It has been suggested to have peptidyltransferase activity; this is somewhat controversial. Makes several contacts with the 16S TRNA in the 70S
                                                                                                                                                                                             1 MALKKYKPITNGRRNMTTLDFAEITKTTPEKSLLQPLPKRAGRNNQGKLTVRHHGGGHKR
                                                                                                                                                                           61 QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVES
                                                                                                                                                                                                                                                                                                         181 GEVRMILSTCRATIGQVGNLQHELVNVGKAGRSRWKGIRPTVRGSVMNPNDHPHGGGGGR
                                                                                                              1 MAIKKYKPITNGRRNMTSLDFAEITKTTPEKSLLKPLPKKAGRNNOGKLTVRHHGGGHKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ribosome (By similarity).
SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the
                                                                                Gaps
                                                                                                                                                                                          ==
Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding. SEQUENCE 277 AA; 30213 MW; CB9D5D88942CD84C CRC64;
                                                                               ;
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                                               DB 1; Length 277;
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                                                                               4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      239 APIGRPSPWSPWGKPTLGKKTRRGKKSSDKLIVRGRKKK 277
                                         Query Match 94.3%; Score 1373; DB 1
Best Local Similarity 93.9%; Pred. No. 2e-99;
Matches 262; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P60425; 0927L0;
29-MRR-2004 (Rel. 43, Created)
29-MRR-2004 (Rel. 43, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50S ribosomal protein L2.
Name=rplB; OrderedLocusNames=lin2778;
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STRAIN=EGD-e / Servar 1/2a;

MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;

A claser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

Charbit A., Chetcuani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Chetcuani F., Couve E., de Daruvar A., Dehoux P.,

Brian K.-D., Fsihi H., Garcia-cled Portillo F., Garrido P., Santian K.-D., Fsihi H., Ganz-Lopez N., Hain T., Hauf J., Jackson D.,

A double E., Matcurnam A., Mata Vicente J., Ng E., Nedjari H.,

Nordisek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simces N., Tierrez A.,

Remmel B., Rose M., Schlueter T., Simces N., Tierrez A.,

Rodarative genomics of Listeria species.";

Science 294:849-852(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 QYRVIDPKRNXDGIPGRVATIEYDPNRSANIALINYADGEKR--YIIAAKGLEVGQTIYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAIKKYKPTTNGRRHMTSSDFAEITTSTPEKSLLRPLKKKAGRNNQGKLTVRHHGGGHKR
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                                                                 EMBL; ALS96173; CAC98004.1; -.
PIR, AD1779; AD1779.
ListList; LIN02778; -.
HAMAP; MF_01320; -; 1.
InterPro; IPR002371; Ribosomal_L2.
InterPro; IPR005880; Ribosomal_L2 b/o.
TIGRFAMS; TIGR01171; rplB_bact; 1.
PROSITE; PS00467; RIBOSOMAL_L2; 1.
Complete proteome; Ribosomal_protein; RNA-binding; RNA-binding.
SEQUENCE 277 AA; 30505 MM; DD0D5B498AFSA632 CRC64;
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(7)
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No. 4.2e-86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1203;
email to license@isb-sib.ch)
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29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 45, Last seq
25-OCT-2004 (Rel. 45, Last ann
50S ribosomal protein L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                       82.68;
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Matches 230; Conservative
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Rembl. BK571885; CAG41311.1; --
Rembl. BK571885; C
                                                                                                                                                           QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVES 120
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                                                                                                       1 MAIKKYKPITNGRRNMTSLDFAEITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
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                                                                              1 MAIKKYKPITNGRRNMTSLDPABITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
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97.0%; Score 1412; DB 2; Length 277; 98.2%; Pred. No. 1.8e-102; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR008994; Nucleic acid OB.
InterPro; IPR008171; Ribosomal L2.
InterPro; IPR00891; Ribosomal L2 b/o.
InterPro; IPR008991; Ribosomal L2; 1.
Pfam; PF03947; Ribosomal L2; 1.
Pfam; PF03947; Ribosomal L2; 1.
PROSTIS; PS00467; RIBOSOMAL L2; 1.
COMplete proceeme; Ribosomal protein.
Complete 277 AA; 30155 MW; F29296D3EBIB146E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  241 APIGRPSPMSPWGKPTLGKKTRRGKKSSDKLIVRGRKKK 279
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus (strain MRSA252).
Bacteria, Firmicutes, Bacillales; Staphylococcus.
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Name=rplB; OrderedLocusNames=SAR2332;
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                    Local Similarity 98.2
hes 274; Conservative
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SEQUENCE FROM N.A.

STRAIN-ATCC 12228;

WEDLINE-22832016; PubMed=12950922;

A Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,

A Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,

A Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,

A Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,

A Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,

A Can Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;

I "Genome-based analysis of virulence genes in a non-biofilm-forming RT Teaphylococcus epidermidis strain (ATCC 12228).";

Mol. Microbiol. 49:1577-1593 (2003).

I FUNCTION: One of the primary PRNA binding proteins Required for association of the 30S and 50S subunit to form the 70S ribosome, controversial. Makes several contacts with the 16S rRNA in the 70S or trobesome (By similarity).

I Thosome (By similarity).

I Thosome (By similarity).

I SIBUNIT: Part of the 50S ribosome (By similarity).

I SIMILARITY: Belongs to the ribosomal protein L2P family.
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                                                                                                                                                  QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVES
    MAIKKYKPITNGRRNMTSLDFAEITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
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Bacteria, Firmicutes; Bacillales; Staphylococcus.
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Last annotation update)
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InterPro; IPR008994; Nucleic acid OB.
InterPro; IPR008994; Nucleic acid OB.
InterPro; IPR0080911; Ribosomal L2.
InterPro; IPR008991; Transl SH3 Ilke.
Pfam; PF00181; Ribosomal L2; 1.
Pfam; PF03947; Ribosomal L2; 1.
TIGREAMS; TIGR01171; rplB bact; 1.
PROSITE; PS00467; RIBOSOMĀL L2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE016750; AA005462.1; -.
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97.0%;
98.2%;
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OrderedLocusNames=SAS2138,
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                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                            119 GAEADIKVGNALPLQNIPVGTVVHNIELKPGKGGQIARSAGASAQVLGKEGKYVLIRLRS
                                                                                                                                                                       61 QYRVIDFYRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVES
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                                                                                                  1 MAIKKYKPITNGRRNMTSLDFAEITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5; Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iamama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramateu K.; Rifamateu K.; Genome and virulence determinants of high virulence community-
                                                                    Gaps
                                                                   2;
                                   Length 277;
                                                                   Indels
 30155 MW; F29296D3EE1E146E CRC64;
                                                                                                                                                                                                                                                                                                                                                                              241 APIGRPSPMSPWGKPTLGKKTRRGKKSSDKLIVRGRKKK 279
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29-MRA-2004 (Rel. 43, Created)
25-MRA-2004 (Rel. 43, Last sequence update)
25-MRA-2004 (Rel. 45, Last annotation update)
50S ribosomal protein L2.
Name-rpla, OrderedLocusAmace=MW2166;
Staphylococcus aureus (strain MW2).
                                 97.0%; Score 1412; DB 1; 98.2%; Pred. No. 1.8e-102;
                                                                   1; Mismatches
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HAMAP; MF_01320; -; 1.
InterPro; IPR002171; Ribosomal_L2.
InterPro; IPR005880; Ribosomal_L2_b/o.
TIGRPAMS; TIGR01171; rplB bact; 1.
PROSITE; PS00467; RIBOSOMĀL_L2; 1.
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                                 Query Match
Best Local Similarity 98.23
Matches 274; Conservative
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277 AA;
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                                                                                                                                                                                                                                                                Gaps
Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding SEQUENCE 277 AA; 30155 MW; P29296D3EE1E146E CRC64;
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Complete proteome; Ribosomal protein.
SEQUENCE 277 AA; 30155 MW; F29296D3EE1E146E CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282459;
                                                                                                                                                          Score 1412; DB 1;
Pred. No. 1.8e-102;
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InterPro; IPR002171; Ribosomal_L2
InterPro; IPR005881; Ribosomal_L2 b/o.
InterPro; IPR00891; Trans1_SH3_I]ke.
Pfam; PF00181; Ribosomal_L2; 1.
Pfam; PF01847; Ribosomal_L2; 1.
IGRPAMs; IIGR01171; rplB_bact; 1.
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Balaban N.;
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                                                                                                          61 QYRVIDFKRNKDGINAKVDSIQYDPNRSANIALVVYADGEKRIYHCIAPKGLEVGQIVES 120
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-i- SUBBUIT: Part of the 50S ribosomal subunit. Forms a bridge to the 30S subunit in the 70S ribosome (By similarity).
-i- SIMILARITY: Belongs to the ribosomal protein L2P family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2; Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; "Whole genome sequencing of meticillin-resistant Staphylococcus
                                             1 MAIKKYKPITNGRRNMTSLDFAEITKTTPEKSLLKPLPKKAGRNNQGKLTVRHHGGGHKR
                                                              1 MAIKKYKPITNGRRNMTSLDFAEITKTTPEKSLLKPLPKKAGRNNOGKLTVRHHGGGHKR
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                2; Gaps
                Indels
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Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
98.2%; Pred. No. 1.8e-102;
                                                                                                                                                                                                                                                                                                                                                                                                      RIZ STAAN STANDARD; PRT; 277 AA P60432; Q99524; Q9AJ03; 29-MAR-2004 (Rel. 43, Created) 29-MAR-2004 (Rel. 43, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation updat 50S ribosomal protein L2
             1; Mismatches
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InterPro; IPR002171; Ribosomal L2.
InterPro; IPR005880; Ribosomal L2_b/o.
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HSSP; P04257; IRL2.
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                Matches 274; Conservative
Best Local Similarity
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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TIGRFAMS; TIGRO1171; rplB_bact; 1.
PROSTIE; PS00467; RIBOSOWAL L2; 1.
Complete proteome; Ribosowal protein; RNA-binding; rRNA-binding.
SEQUENCE 277 AA; 30155 WW; F29296D3EE1E146E CRC64;
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                                                                                                                                                                 Length 277;
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                                                                                                                                                              Score 1412; DB 1;
Pred. No. 1.8e-102;
1; Mismatches 2;
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InterPro; IPR002171; Ribosomal_L2.
InterPro; IPR00580; Ribosomal_L2_b/o.
TIGRFAMS; TIGR01171; TplB bact; 1.
PROSTE; P800467; RIBOSOWAL L2; 1.
Ribosomal protein; RNA-binding; rRNA-binding.
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Best Local Similarity 98.2%;
Matches 274; Conservative
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GenCore version 5.1.6
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RL2 BACCR
7,2 BACST
STRP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RL2_STAEP
RL2_LISIN
RL2_LISMO
Q71WE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O65PA4
RL2 BACSU
RL2 OCEIH
RL2 BACHD
RL2 BACHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RL2_STAAM
RL2_STAAN
RL2_STAAU
RL2_STAAW
Q6G774
Q6GE16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENTFA
                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0
seq length: 200000000
                                                                                                                                                                                             US-09-839-695B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UniProt 03:*
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               June
                                                                                                                                                                                                               1456
                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1412
1412
1412
1203
1203
11203
11158
11158
11139
11139
11139
11137
11137
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                                                                                                                                                                                                                                                                       Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB E
Maximum DB E
                                                                             OM protein
                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                   о
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mesoplasma
symbiobacte
clostridium
                mycoplasma
clostridium
       onion yello
aster yello
                                         spiroplasma
                                                 clostridium
                                     mycoplasma
                                              mycoplasma
                                                      mycoplasma
   Q8ge24
P60402
Q50264
               089m57
097eil
06flzl
067ju6
08xh86
06msm8
P60404
                                                 0890p1
098py4
       RL2_ONYPE
RL2_ASTYP
RL2_MYCHO
RL2_CLOAB
Q6FTZ1
Q67JU6
RL2_CLOPE
Q67JU6
                                         RL2 SPIKU
Q6KI52
                                                 RL2 CLOTE
RL2 MYCPU
994
975.5
964.5
964.5
953
953
954
954
954
954
954
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ALIGNMENTS

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RESULT 1

RESULT 1

RESULT 1

RESULT 1

DE 12.5TAPA

NEW PRODITION CONTROLLED 12.

RESULT TAXAD-15809 M.A.

REDITION TAXAD-15809 M.A.

REDITION TO THE 12.5TAPA M.A.

RA MAINTEN TO THE 12.TAPA M.A.

RA MAINTEN TO THE 12.TAPA M.A.

RA MAINTEN TO THE 12.TAPA M.A.

R
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